

**Table S1. Average differential expression ratio (ATPase vs vector control).**

Gene	CtcC ATPase		E242A ATPase <sup>a</sup>	CtcC Full Length
	RNAseq	ddPCR		
<i>ct084</i>	4.68	28.78	1.42	1.51 <sup>b</sup>
<i>ct105</i>	3.12	3.41	-1.17	1.43 <sup>b</sup>
<i>ct142</i>	4.81	13.14	1.29	1.51 <sup>b</sup>
<i>ct229</i>	3.67	9.11	1.18	1.47 <sup>b</sup>
<i>ct394</i>	4.50	9.67	1.50	1.98 <sup>b</sup>
<i>ct444</i>	4.60	22.16	1.02	1.77 <sup>b</sup>
<i>ct456</i>	4.75	4.66	-1.47	2.70 <sup>c</sup>
<i>ct494</i>	5.02	27.35	1.04	1.76 <sup>b</sup>
<i>ct576</i>	4.83	5.10	1.09	1.31 <sup>b</sup>
<i>ct619</i>	5.66	3.53	1.00	4.71 <sup>c</sup>
<i>ct620</i>	6.48	27.61	1.40	5.92 <sup>b</sup>
<i>ct646</i>	4.32	2.98	1.01	1.55
<i>ct683</i>	3.59	4.65	1.06	2.21 <sup>b</sup>
<i>ct711</i>	4.36	7.19	1.15	5.42 <sup>c</sup>
<i>ct814</i>	3.55	6.08	1.13	1.32 <sup>b</sup>
<i>ct814.1</i>	5.24	12.47	-1.39	1.21 <sup>b</sup>
<i>ct847</i>	4.03	8.00	1.79	1.66 <sup>b</sup>
<i>ct875</i>	3.83	3.17	1.07	2.39
<i>hctB</i>	3.31	2.99	1.00	2.70
<i>rpoA</i>	-1.33	-1.08	1.12	1.05

<sup>a</sup> All genes analyzed by ddPCR for the CtcC ATPase E242A mutant had significantly different transcription levels, with the exception of the *rpoA* control (p-value <0.05).

<sup>b</sup> Significant differences in transcript counts for selected genes between the Full-length CtcC and the CtcC ATPase domain-only expression variants by ddPCR analysis (p-value <0.05).

<sup>c</sup> Significant differences in transcript counts for selected genes between the Full-length CtcC and the CtcC ATPase E242A mutant expression variants by ddPCR analysis (p-value <0.05).